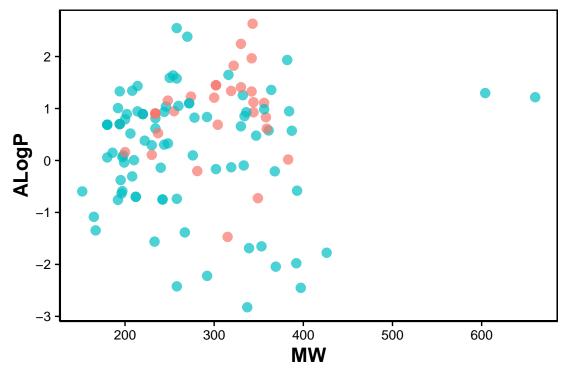
Chemical Space

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Chemical space of anti-sickling

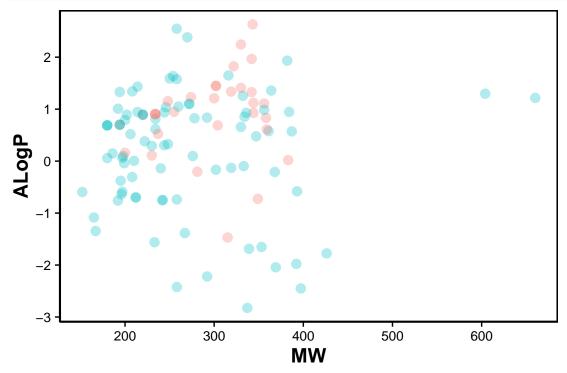
```
library(cowplot)
data <- read.csv("Linpiski_Descriptors.csv")</pre>
descriptors_name <- c("ALogP", "nHBAcc", "nHBDon", "MW")</pre>
descriptors <- data[, descriptors_name]</pre>
Activity <- data$Activity</pre>
data_2 <- cbind(Activity, descriptors)</pre>
data_plot <- data.frame(data_2)</pre>
p <- ggplot(data_plot, aes(MW, ALogP))</pre>
p <- p + geom_point(aes(colour = factor(Activity)), size = 3, alpha = 0.7)</pre>
p <- p + theme(legend.position = ("none"),</pre>
                 panel.border = element_rect(linetype = "solid",
                                               colour = "black", fill = NA, size = 1),
                 axis.text.x = element_text(colour = "black", size = 10),
                 axis.text.y = element_text(colour = "black", size = 10),
                 plot.margin = grid::unit(c(1, 1, 1, 1), "cm"),
                 axis.title.x = element_text(colour = "black", size = 15, face = "bold"),
                 axis.title.y = element_text(colour = "black", size = 15, face = "bold"))
print(p)
```



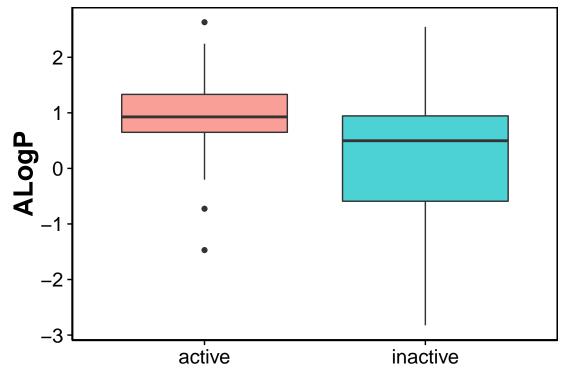
Visualization of Lipinski's descriptors

Chemical space of AChE inhibitors are shown as active (green), inactive (red) and intermediate (blue)

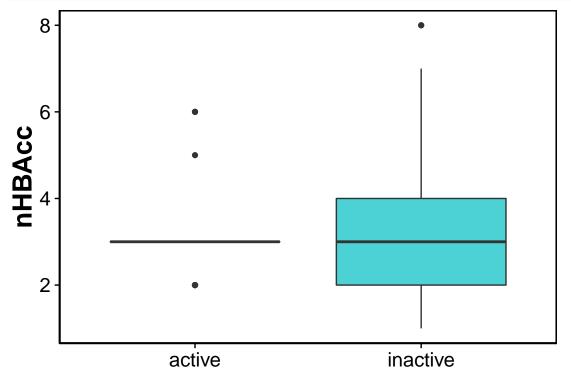
```
library(ggplot2)
library(cowplot)
data_2 <- cbind(Activity, descriptors)</pre>
data_2 <- na.omit(data_2)</pre>
data_plot <- data.frame(data_2)</pre>
p <- ggplot(data_plot, aes(MW, ALogP))</pre>
p <- p + geom_point(aes(colour = factor(Activity)), size = 3, alpha = 0.3)
p <- p + theme(legend.position = ("none"),</pre>
           panel.border = element_rect(linetype = "solid",
                                         colour = "black", fill = NA, size = 1),
           axis.text.x = element_text(colour = "black", size = 10),
           axis.text.y = element_text(colour = "black", size = 10),
           plot.margin = unit(c(1, 1, 1, 1), "cm"),
           axis.title.x = element_text(colour = "black", size = 15, face = "bold"),
           axis.title.y = element_text(colour = "black", size = 15, face = "bold")
print(p)
```



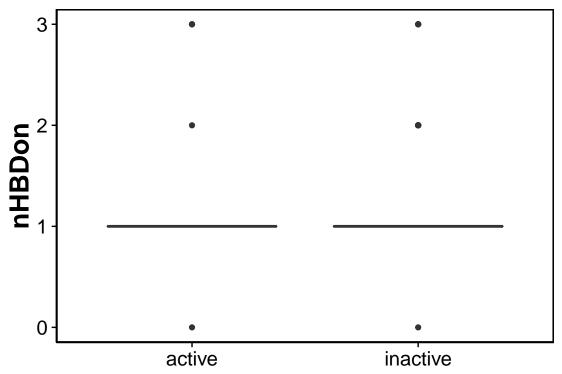
Boxplot of Lipinski's rule-of-five descriptors (ALogP)



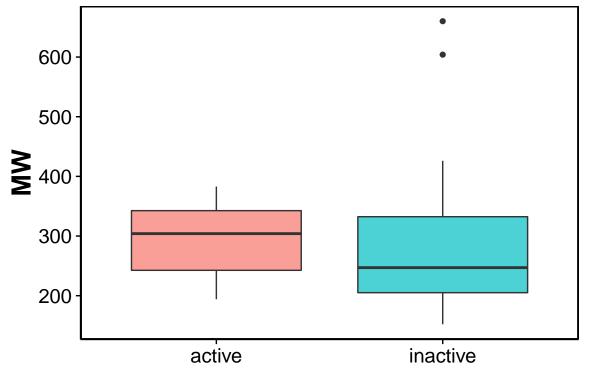
Boxplot of Lipinski's rule-of-five descriptors (nHBAcc)



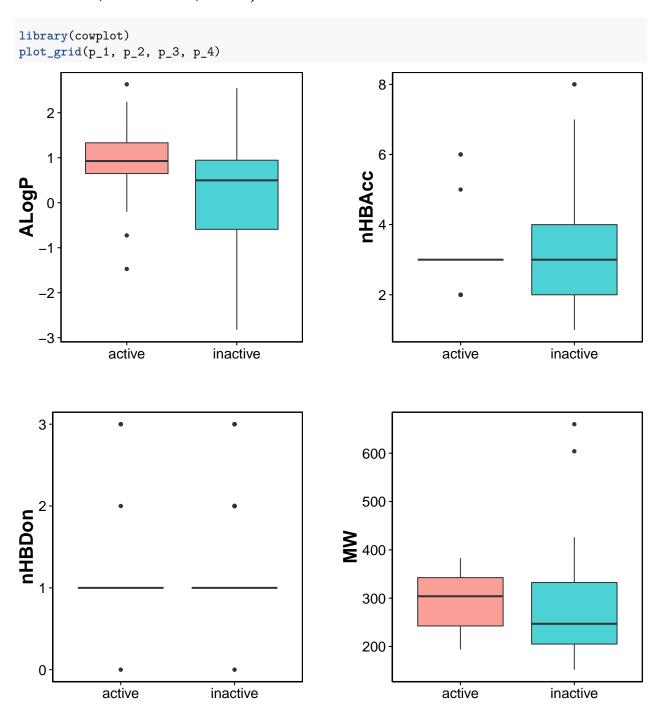
Boxplot of Lipinski's rule-of-five descriptors (nHBDon)



Boxplot of Lipinski's rule-of-five descriptors (MW)



Arranging boxplot of Lipinski's rule-of-file descriptors (ALogP, nHBAcc, nHBDon, MW)



EDA of feature important analysis

```
library(caret)
library(reshape2)
```

```
df <- read.csv("data.csv")</pre>
names <- c("Activity", "SubFPC171", "SubFPC5", "SubFPC1", "SubFPC298", "SubFPC2", "SubFPC16", "SubFPC17
            "SubFPC100")
df <- df[, names]</pre>
data_melt <- melt(df)</pre>
ggplot(aes(y = value, x = variable, fill = Activity), data = data_melt) + geom_boxplot() +
  ylab("Substructure Count") + theme(
    legend.position = "none",
    axis.text.y = element_text(size = 20, colour = "black"),
    axis.text.x = element_text(size = 20, colour = "black"),
    plot.margin = unit(c(1,1, 1, 1), "cm"),
    panel.border = element_rect(linetype = "solid", colour = "black", fill = NA, size = 1),
    axis.title = element_text(size = 25, face = "bold", colour = "black")
Substructure Count
    SubFPC171
                       SubFPC1
                                SubFPC298
                                                  SubFPC16
                                                           SubFPC173 SubFPC18 SubFPC275 SubFPC100
                                          SubFPC2
```

variable